

1635  
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 #13  
 2-5-02  
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## RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/600,535

DATE: 01/16/2002

TIME: 13:04:13

Input Set : A:\Sim.app

Output Set: N:\CRF3\01162002\I600535.raw

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3 <110> APPLICANT: Sims, Peter J.
4     Zhao, Ji
5     Wiedmer, Therese
7 <120> TITLE OF INVENTION: METHODS AND COMPOSITIONS TO ALTER TISSUE SUSCEPTIBILITY
8     TO IMMUNE INJURY, TO PROGRAMMED CELL DEATH, AND TO
9     CLEARANCE BY THE RETICULOENDOTHELIAL SYSTEM
11 <130> FILE REFERENCE: 160180.90121
C--> 13 <140> CURRENT APPLICATION NUMBER: US/09/600,535
C--> 14 <141> CURRENT FILING DATE: 2000-07-18
16 <160> NUMBER OF SEQ ID NOS: 9
18 <170> SOFTWARE: PatentIn Ver. 2.0
20 <210> SEQ ID NO: 1
21 <211> LENGTH: 1445
22 <212> TYPE: DNA
23 <213> ORGANISM: Homo sapiens
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28 cagaagagga agccatcgcc tggccccggc tctctggacc ttgtctcgct cgggagcgga 180
29 aacagcgcca gccagagaac tgttttaatc atggacaaac aaaactcaca gatgaatgct 240
30 tctcaccggg aaacaaactt gccagttggg tctcctctc agtatccacc gacagcattc 300
31 caaggacctc caggatatag tggctacctt gggccccagg tcagctaccc acccccacca 360
32 gccggccatt caggctcttg cccagctggc tttcctgtcc caaatcagcc agtgtataat 420
33 cagccagtat ataatcagcc agttggagct gcaggggtac catggatgcc agcgccacag 480
34 cctccattaa actgtccacc tggattagaa tatttaagtc agatagatca gatactgatt 540
35 catcagcaaa ttgaacttct ggaagtttta acaggttttg aaactaataa caaatatgaa 600
36 attaagaaca gctttggaca gagggtttac tttgcagcgg aagatactga ttgctgtacc 660
37 cgaaattgct gtgggccatc tagacctttt accttgagga ttattgataa tatgggtcaa 720
38 gaagtcataa ctctggagag accactaaga tgtagcagct gttgttgtcc ctgctgcctt 780
39 caggagatag aaatccaagc tctcctgtgt gtaccaatag gttatgttat tcagacttgg 840
40 caccatgtc taccaaagtt tacaattcaa aatgagaaaa gagaggatgt actaaaaata 900
41 agtgggtccat gtgttgtgtg cagctgttgt ggagatgttg attttgagat taaatctctt 960
42 gatgaacagt gtgtggttgg caaaatttcc aagcactgga ctggaatttt gagagaggca 1020
43 ttacagacg ctgataactt tggaatccag ttccctttag accttgatgt taaaatgaaa 1080
44 gctgtaata ga ttggtgcctg tttcctcatt gacttcatgt ttttgaaaag cactggcagc 1140
45 caggaacaaa aatcaggagt gtggtagtgg attagtgaat gtctcctcag gaaatctgaa 1200
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48 tataaagggt tttgtacatt ttttaatact cattgtcaat ttgagaaaaa ggacatatga 1380
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50 gccgc
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53 <211> LENGTH: 318
54 <212> TYPE: PRT
55 <213> ORGANISM: Homo sapiens
57 <400> SEQUENCE: 2
58 Met Asp Lys Gln Asn Ser Asn Met Asn Ala Ser His Pro Glu Thr Asn

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59      1              5              10              15
61 Leu Pro Val Gly Tyr Pro Pro Asn Tyr Pro Pro Thr Ala Phe Gln Gly
62              20              25              30
64 Pro Pro Gly Tyr Ser Gly Tyr Pro Gly Pro Gln Val Ser Tyr Pro Pro
65              35              40              45
67 Pro Pro Ala Gly His Ser Gly Pro Gly Pro Ala Gly Phe Pro Val Pro
68              50              55              60
70 Asn Gln Pro Val Tyr Asn Gln Pro Val Tyr Asn Gln Pro Val Gly Ala
71 65              70              75              80
73 Ala Gly Val Pro Trp Met Pro Ala Pro Gln Pro Pro Leu Asn Cys Pro
74              85              90              95
76 Pro Gly Leu Glu Tyr Leu Ser Gln Ile Asp Gln Ile Leu Ile His Gln
77              100              105              110
79 Gln Ile Glu Leu Leu Glu Val Leu Thr Gly Phe Glu Thr Asn Asn Lys
80              115              120              125
82 Tyr Glu Ile Lys Asn Ser Phe Gly Gln Arg Val Tyr Phe Ala Ala Glu
83              130              135              140
85 Asp Thr Asp Cys Cys Thr Arg Asn Cys Cys Gly Pro Ser Arg Pro Phe
86 145              150              155              160
88 Thr Leu Arg Ile Ile Asp Asn Met Gly Gln Glu Val Ile Thr Leu Glu
89              165              170              175
91 Arg Pro Leu Arg Cys Ser Ser Cys Cys Cys Pro Cys Cys Leu Gln Glu
92              180              185              190
94 Ile Glu Ile Gln Ala Pro Pro Gly Val Pro Ile Gly Tyr Val Ile Gln
95              195              200              205
97 Thr Trp His Pro Cys Leu Pro Lys Phe Thr Ile Gln Asn Glu Lys Arg
98              210              215              220
100 Glu Asp Val Leu Lys Ile Ser Gly Pro Cys Val Val Cys Ser Cys Cys
101 225              230              235              240
103 Gly Asp Val Asp Phe Glu Ile Lys Ser Leu Asp Glu Gln Cys Val Val
104              245              250              255
106 Gly Lys Ile Ser Lys His Trp Thr Gly Ile Leu Arg Glu Ala Phe Thr
107              260              265              270
109 Asp Ala Asp Asn Phe Gly Ile Gln Phe Pro Leu Asp Leu Asp Val Lys
110              275              280              285
112 Met Lys Ala Val Met Ile Gly Ala Cys Phe Leu Ile Asp Phe Met Phe
113              290              295              300
115 Phe Glu Ser Thr Gly Ser Gln Glu Gln Lys Ser Gly Val Trp
116 305              310              315
119 <210> SEQ ID NO: 3
120 <211> LENGTH: 1622
121 <212> TYPE: DNA
122 <213> ORGANISM: Mus musculus
124 <400> SEQUENCE: 3
125 tctaaagact caggaaacaa aacctaaatt gcctcaaagt tcaggtgctt tttctccctg 60
126 acttttagtct agtggagtag tgcagcacct atgcctttct gagaggagtc tggagagctg 120
127 agtcgctgct ggtgctagga ttctaggaat tcgcctcact tggagctgca tgagaaaaga 180
128 aaggcttgca aatggaggct cctcgctcag gaacatactt gccagctggg tatgcccctc 240
129 agtatcctcc agcagcagtc caaggacctc cagagcatac tggacgcccc acattccaga 300

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130 ctaactacca agttccccag tctggttata caggacctca ggctagctac acagtctcaa 360
131 catctggaca tgaaggttat gctgctacac ggcttcctat tcaaaataat cagactatag 420
132 tccttgcaaa cactcagtg atgccagcac caccacctat tctgaactgc ccacctgggc 480
133 tagaatactt aaatcagata gatcagcttc tgattcatca gcaagttgaa cttctagaag 540
134 tcttaacagg ctttgaaaca aataacaaat ttgaaatcaa gaacagcctc gggcagatgg 600
135 tttatgttgc agtggaaagat actgactgct gtactcgaaa ttgctgtgaa gcgtctagac 660
136 ctttcacctt aagaatcctg gatcatctgg gccagaagt catgactctg gagcgacctc 720
137 tgagatgcag tagctgtctg ttccctgtct gcctccagga gatagaaatc caggctcctc 780
138 cgggggtgcc aataggttat gtgactcaga cctggcacc atgtctgcca aagctcactc 840
139 ttcagaacga caagaggag aatgttctaa aagtagttgg tccatgtgtt gcatgcacct 900
140 gctgttcaga tattgacttt gagatcaagt ctcttgatga agtgactaga attggtaaga 960
141 tcaccaagca gtggtctggt tgtgtgaaag aggccttcac ggattcggat aactttggga 1020
142 tccaattccc gctagacctg gaggtgaaga tgaaagctgt gacgcttggt gcttgcttcc 1080
143 tcatagatta catgtttttt gaaggctgtg agtaggaaca gaaatccgac ctgcagtagg 1140
144 aatcaatgaa agaggacaga gaagatctga agtctacaca aggagatcat atgattgaga 1200
145 gacctggggc tttttgattt cttcattgaa atttctcaga atcaagctgt tacaatgaa 1260
146 gcatagtatg taacattttg gttttcaa atgtagtttat cttttacatt attggaatag 1320
147 acctggataa ttatctttat acacttctaa aaatatgcac caaattcaag ttaaaaaaaa 1380
148 aaagacgaag agaagtgtat gttttaaaat aaaacatttt atggaaaagt aagttaaata 1440
149 ataactctgg atttattttt catcttttgt tcaatttaaa ccttgttagt gctgatttta 1500
150 ttataaaaatt gtactttact atcaaaccta gttagtttat ttcttacaga aatcctccta 1560
151 ttattttgaa attacatatt tttgaaagct ttttaaaaga tactattgcc tgggaaattc 1620
152 ta

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154 &lt;210&gt; SEQ ID NO: 4

155 &lt;211&gt; LENGTH: 307

156 &lt;212&gt; TYPE: PRT

157 &lt;213&gt; ORGANISM: Mus musculus

159 &lt;400&gt; SEQUENCE: 4

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160 Met Glu Ala Pro Arg Ser Gly Thr Tyr Leu Pro Ala Gly Tyr Ala Pro
161 1 5 10 15
163 Gln Tyr Pro Pro Ala Ala Val Gln Gly Pro Pro Glu His Thr Gly Arg
164 20 25 30
166 Pro Thr Phe Gln Thr Asn Tyr Gln Val Pro Gln Ser Gly Tyr Pro Gly
167 35 40 45
169 Pro Gln Ala Ser Tyr Thr Val Ser Thr Ser Gly His Glu Gly Tyr Ala
170 50 55 60
172 Ala Thr Arg Leu Pro Ile Gln Asn Asn Gln Thr Ile Val Leu Ala Asn
173 65 70 75 80
175 Thr Gln Trp Met Pro Ala Pro Pro Pro Ile Leu Asn Cys Pro Pro Gly
176 85 90 95
178 Leu Glu Tyr Leu Asn Gln Ile Asp Gln Leu Leu Ile His Gln Gln Val
179 100 105 110
181 Glu Leu Leu Glu Val Leu Thr Gly Phe Glu Thr Asn Asn Lys Phe Glu
182 115 120 125
184 Ile Lys Asn Ser Leu Gly Gln Met Val Tyr Val Ala Val Glu Asp Thr
185 130 135 140
187 Asp Cys Cys Thr Arg Asn Cys Cys Glu Ala Ser Arg Pro Phe Thr Leu
188 145 150 155 160
190 Arg Ile Leu Asp His Leu Gly Gln Glu Val Met Thr Leu Glu Arg Pro

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191          165          170          175
193 Leu Arg Cys Ser Ser Cys Cys Phe Pro Cys Cys Leu Gln Glu Ile Glu
194          180          185          190
196 Ile Gln Ala Pro Pro Gly Val Pro Ile Gly Tyr Val Thr Gln Thr Trp
197          195          200          205
199 His Pro Cys Leu Pro Lys Leu Thr Leu Gln Asn Asp Lys Arg Glu Asn
200          210          215          220
202 Val Leu Lys Val Val Gly Pro Cys Val Ala Cys Thr Cys Cys Ser Asp
203 225          230          235          240
205 Ile Asp Phe Glu Ile Lys Ser Leu Asp Glu Val Thr Arg Ile Gly Lys
206          245          250          255
208 Ile Thr Lys Gln Trp Ser Gly Cys Val Lys Glu Ala Phe Thr Asp Ser
209          260          265          270
211 Asp Asn Phe Gly Ile Gln Phe Pro Leu Asp Leu Glu Val Lys Met Lys
212          275          280          285
214 Ala Val Thr Leu Gly Ala Cys Phe Leu Ile Asp Tyr Met Phe Phe Glu
215          290          295          300
217 Gly Cys Glu
218 305

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221 &lt;210&gt; SEQ ID NO: 5

222 &lt;211&gt; LENGTH: 14

223 &lt;212&gt; TYPE: PRT

224 &lt;213&gt; ORGANISM: Artificial Sequence

226 &lt;220&gt; FEATURE:

227 &lt;223&gt; OTHER INFORMATION: Fragment of SEQ ID NO:2

229 &lt;400&gt; SEQUENCE: 5

230 Cys Glu Ser Thr Gly Ser Gln Glu Gln Lys Ser Gly Val Trp

231 1 5 10

234 &lt;210&gt; SEQ ID NO: 6

235 &lt;211&gt; LENGTH: 39

236 &lt;212&gt; TYPE: DNA

237 &lt;213&gt; ORGANISM: Artificial Sequence

239 &lt;220&gt; FEATURE:

240 &lt;223&gt; OTHER INFORMATION: Primer for SEQ ID NO:1

242 &lt;400&gt; SEQUENCE: 6

243 tcagaattcg gatccatgga caaacaaaac tcacagatg

39

245 &lt;210&gt; SEQ ID NO: 7

246 &lt;211&gt; LENGTH: 43

247 &lt;212&gt; TYPE: DNA

248 &lt;213&gt; ORGANISM: Artificial Sequence

250 &lt;220&gt; FEATURE:

251 &lt;223&gt; OTHER INFORMATION: Primer for SEQ ID NO:1

253 &lt;400&gt; SEQUENCE: 7

254 gcttgctgc aggtcgacct accacactcc tgatttttgt tcc

43

256 &lt;210&gt; SEQ ID NO: 8

257 &lt;211&gt; LENGTH: 38

258 &lt;212&gt; TYPE: DNA

259 &lt;213&gt; ORGANISM: Artificial Sequence

261 &lt;220&gt; FEATURE:

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DATE: 01/16/2002

PATENT APPLICATION: US/09/600,535

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Input Set : A:\Sim.app

Output Set: N:\CRF3\01162002\I600535.raw

262 &lt;223&gt; OTHER INFORMATION: Primer for SEQ ID NO:3

264 &lt;400&gt; SEQUENCE: 8

265 tcagaattcg gatccatgga ggctcctcgc tcaggaac

38

267 &lt;210&gt; SEQ ID NO: 9

268 &lt;211&gt; LENGTH: 43

269 &lt;212&gt; TYPE: DNA

270 &lt;213&gt; ORGANISM: Artificial Sequence

272 &lt;220&gt; FEATURE:

273 &lt;223&gt; OTHER INFORMATION: Primer for SEQ ID NO:3

275 &lt;400&gt; SEQUENCE: 9

276 gcttgctgc aggtcgacct acacacagcc ttcaaaaaaac tag

43

VERIFICATION SUMMARY

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